

## SEQUENCE LISTING

<110> Novak, Julia E.  
Presnell, Scott R.  
Sprecher, Cindy A.  
Foster, Donald C.  
Holly, Richard D.  
Gross, Jane A.  
Johnston, Janet V.  
Nelson, Andrew J.  
Dillon, Stacey R.  
Hammond, Angela K.

<120> NOVEL CYTOKINE ZALPHA11 LIGAND

<130> 99-16

<150> US 60/123,547  
<151> 1999-03-09

<150> US 60/123,904  
<151> 1999-03-11

<150> US 60/142,013  
<151> 1999-07-01

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Ser Pro Gly Asn Met Glu Arg Ile Val Ile Cys Leu Met Val Ile Phe	
5 10 15	
ttg ggg aca ctg gtc cac aaa tca agc tcc caa ggt caa gat cgc cac	151
Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln Asp Arg His	
20 25 30 35	
atg att aga atg cgt caa ctt ata gat att gtt gat cag ctg aaa aat	199
Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln Leu Lys Asn	
40 45 50	
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Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro Glu Asp Val	
55 60 65	
gag aca aac tgt gag tgg tca gct ttt tcc tgt ttt cag aag gcc caa	295
Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln Lys Ala Gln	
70 75 80	
cta aag tca gca aat aca gga aac aat gaa agg ata atc aat gta tca	343
Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile Asn Val Ser	
85 90 95	
att aaa aag ctg aag agg aaa cca cct tcc aca aat gca ggg aga aga	391
Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala Gly Arg Arg	
100 105 110 115	
cag aaa cac aga cta aca tgc cct tca tgt gat tct tat gag aaa aaa	439
Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr Glu Lys Lys	
120 125 130	
cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc caa aag atg	487
Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu Gln Lys Met	
135 140 145	
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Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu Asp Ser	
150 155 160	

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Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln
35     40     45
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro
50     55     60
Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln
65     70     75     80
Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile
85     90     95
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100    105    110
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr
115    120    125
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu
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aargncary	tnaarwsngc	naayacnggn	aayaaygarm	gnathathaa	ygtwnsnath	300
aaraarytna	armgnaarcc	nccnwsnacn	aaygcnggnm	gnmgncaraa	rcaymgnytn	360
acntgyccnw	sntgygayws	ntaygaraar	aarccncna	argarttyyt	ngarmgntty	420
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aaaaaatatt	atttaaattg	cattgtgaca	aacatggcct	taccaagtca	ttttcataga	420
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of Fc4

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agg agg ctg cct gcc agg agg gga gga aag aaa cag aag cac ata gct Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala 100 105 110	392
aaa tgc cct tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe 115 120 125	440
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&lt;211&gt; 146

&lt;212&gt; PRT

<213> mus musculus

<400> 56

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Leu Asp Pro Glu Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys
 50           55           60
Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
 65           70           75           80
Asn Pro Gly Asn Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu
 85           90           95
Arg Arg Arg Leu Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile
 100          105          110
Ala Lys Cys Pro Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu
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32

&lt;210&gt; 63

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&lt;212&gt; DNA

&lt;213&gt; homo sapiens

&lt;400&gt; 63

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caactaaagt cagcaaatac aggaaacaat gaaaggataa tcaatgtatc aattaaaaag	300
ctgaagagga aaccaccttc cacaaatgca gggagaagac agaaacacag actaacatgc	360
ccttcatgtg attcttatga gaaaaaacca cccaaagaat tcctagaaag attcaaatca	420
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&lt;210&gt; 64

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC22052

&lt;400&gt; 64

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57

&lt;210&gt; 65

&lt;211&gt; 57

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC22053

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57

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1

5

10

15

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25

30

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40

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<223> HuzalphallL-3 peptide

<400> 73

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&lt;222&gt; (1)...(1560)

&lt;223&gt; MBP-human zalphal1 Ligand fusion polynucleotide

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Gly	Ile	Lys	Val	Thr	Val	Glu	His	Pro	Asp	Lys	Leu	Glu	Glu	Lys	Phe	
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cca	cag	gtt	gcg	gca	act	ggc	gat	ggc	cct	gac	att	atc	ttc	tgg	gca	192
Pro	Gln	Val	Ala	Ala	Thr	Gly	Asp	Gly	Pro	Asp	Ile	Ile	Phe	Trp	Ala	
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His	Asp	Arg	Phe	Gly	Gly	Tyr	Ala	Gln	Ser	Gly	Leu	Leu	Ala	Glu	Ile	
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Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp	
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Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly	
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aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
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340 345 350	
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Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn	
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370 375 380	
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Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile	
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405 410 415	
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Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala	
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Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro	
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465 470 475 480	

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 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg  
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 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
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 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
   50                    55                    60  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
  65                    70                    75                    80  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
                     85                    90                    95  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
                     100                    105                    110  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
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 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
                     130                    135                    140  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
  145                    150                    155                    160



Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
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 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
 210 215 220  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
 245 250 255  
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
 290 295 300  
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
 305 310 315 320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
 325 330 335  
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 340 345 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
 355 360 365  
 Ser Ser Ser His His His His His Ala Asn Ser Val Pro Leu Val  
 370 375 380  
 Pro Arg Gly Ser Gln Asp Arg His Met Ile Arg Met Arg Gln Leu Ile  
 385 390 395 400  
 Asp Ile Val Asp Gln Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu  
 405 410 415  
 Phe Leu Pro Ala Pro Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala  
 420 425 430  
 Phe Ser Cys Phe Gln Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn  
 435 440 445  
 Asn Glu Arg Ile Ile Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro  
 450 455 460  
 Pro Ser Thr Asn Ala Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro  
 465 470 475 480  
 Ser Cys Asp Ser Tyr Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg  
 485 490 495

Phe Lys Ser Leu Leu Gln Lys Met Ile His Gln His Leu Ser Ser Arg  
                   500                  505                  510  
 Thr His Gly Ser Glu Asp Ser  
                   515

<210> 86  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22849

<400> 86  
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 actt 64

<210> 87  
 <211> 64  
 <212> DNA  
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<220>  
 <223> Oligonucleotide primer ZC22850

<400> 87  
 tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctaggagaga tgctgatgaa 60  
 tcat 64

<210> 88  
 <211> 1533  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> MBP-mouse zalpha11 Ligand fusion polynucleotide

<221> CDS  
 <222> (1)...(1533)

<400> 88

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ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr 20 25 30	96
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe 35 40 45	144
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala 50 55 60	192
cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile 65 70 75 80	240
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp 85 90 95	288
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu 100 105 110	336
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys 115 120 125	384
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly 130 135 140	432
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528

tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys 225 230 235 240	720
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008

atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc cca gat cgc ctc ctg att aga ctt cgt cac ctt att Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile 385 390 395 400	1200
gac att gtt gaa cag ctg aaa atc tat gaa aat gac ttg gat cct gaa Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu 405 410 415	1248
ctt cta tca gct cca caa gat gta aag ggg cac tgt gag cat gca gct Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala 420 425 430	1296
ttt gcc tgt ttt cag aag gcc aaa ctc aag cca tca aac cct gga aac Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn 435 440 445	1344
aat aag aca ttc atc att gac ctc gtg gcc cag ctc agg agg agg ctg Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu 450 455 460	1392
cct gcc agg agg gga gga aag aaa cag aag cac ata gct aaa tgc cct Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro 465 470 475 480	1440
tcc tgt gat tcg tat gag aaa agg aca ccc aaa gaa ttc cta gaa aga Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg 485 490 495	1488
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<210> 89  
 <211> 510  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> MBP-mouse zalpha11 Ligand fusion polypeptide

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 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
 35 40 45  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
 50 55 60  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
 65 70 75 80  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
 85 90 95  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
 100 105 110  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
 115 120 125  
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
 130 135 140  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
 145 150 155 160  
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
 165 170 175  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
 180 185 190  
 Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
 210 215 220  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
 245 250 255

Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
 290 295 300  
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
 305 310 315 320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
 325 330 335  
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
 340 345 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
 355 360 365  
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val  
 370 375 380  
 Pro Arg Gly Ser Pro Asp Arg Leu Leu Ile Arg Leu Arg His Leu Ile  
 385 390 395 400  
 Asp Ile Val Glu Gln Leu Lys Ile Tyr Glu Asn Asp Leu Asp Pro Glu  
 405 410 415  
 Leu Leu Ser Ala Pro Gln Asp Val Lys Gly His Cys Glu His Ala Ala  
 420 425 430  
 Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser Asn Pro Gly Asn  
 435 440 445  
 Asn Lys Thr Phe Ile Ile Asp Leu Val Ala Gln Leu Arg Arg Arg Leu  
 450 455 460  
 Pro Ala Arg Arg Gly Gly Lys Lys Gln Lys His Ile Ala Lys Cys Pro  
 465 470 475 480  
 Ser Cys Asp Ser Tyr Glu Lys Arg Thr Pro Lys Glu Phe Leu Glu Arg  
 485 490 495  
 Leu Lys Trp Leu Leu Gln Lys Met Ile His Gln His Leu Ser  
 500 505 510

<210> 90

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22281

<400> 90

tgtgaatgac ttggtccctg aa

<210> 91  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22279

<400> 91  
 aacaggaaaa agctgaccac tca 23

<210> 92  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human zalphal1 Ligand TaqMan probe, ZG32

<400> 92  
 tctgccagct ccagaagatg tagagacaaa c 31

<210> 93  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22277

<400> 93  
 ccaggagtgt ggcagctttc 20

<210> 94  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC22276

<400> 94



gcttgccctt cagcatgtag a 21

<210> 95  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Human zalpha11 TaqMan probe, ZG31

<400> 95  
 cggtccccc tttcaacgtg act 23

<210> 96  
 <211> 1821  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> CDS  
 <222> (1)...(1821)

<223> MBP-zalpha11 soluble receptor polynucleotide  
 sequence

<400> 96  
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 Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys  
 1 5 10 15

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc 96  
 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr  
 20 25 30

gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc 144  
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
 35 40 45

cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca 192  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
 50 55 60

cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile 65 70 75 80	240
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp 85 90 95	288
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu 100 105 110	336
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys 115 120 125	384
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly 130 135 140	432
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576
ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys 225 230 235 240	720

gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056
agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200

acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc	1248
Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu	
405 410 415	
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc	1296
Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr	
420 425 430	
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac	1344
Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr	
435 440 445	
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt	1392
Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser	
450 455 460	
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc	1440
Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser	
465 470 475 480	
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act	1488
Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr	
485 490 495	
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa	1536
Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu	
500 505 510	
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag	1584
Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln	
515 520 525	
tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg	1632
Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu	
530 535 540	
atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc	1680
Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg	
545 550 555 560	
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc	1728
Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly	
565 570 575	

tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt 1776  
 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe  
                   580                                  585                                  590

cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac tag 1821  
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His \*  
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<210> 97

<211> 606

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP-zalpa11 soluble receptor polypeptide sequence

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 Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr  
                                   20                                  25                                  30  
 Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe  
                                   35                                  40                                  45  
 Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala  
                                   50                                  55                                  60  
 His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile  
 65                                  70                                  75                                  80  
 Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp  
                                   85                                  90                                  95  
 Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu  
                                   100                                  105                                  110  
 Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys  
                                   115                                  120                                  125  
 Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly  
                                   130                                  135                                  140  
 Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro  
 145                                  150                                  155                                  160  
 Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys  
                                   165                                  170                                  175  
 Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly  
                                   180                                  185                                  190

Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp  
 195 200 205  
 Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala  
 210 215 220  
 Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys  
 225 230 235 240  
 Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser  
 245 250 255  
 Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro  
 260 265 270  
 Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp  
 275 280 285  
 Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala  
 290 295 300  
 Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala  
 305 310 315 320  
 Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln  
 325 330 335  
 Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala  
 340 345 350  
 Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn  
 355 360 365  
 Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val  
 370 375 380  
 Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln  
 385 390 395 400  
 Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu  
 405 410 415  
 Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr  
 420 425 430  
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr  
 435 440 445  
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser  
 450 455 460  
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser  
 465 470 475 480  
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr  
 485 490 495  
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu  
 500 505 510  
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln  
 515 520 525

Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu  
 530 535 540  
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg  
 545 550 555 560  
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly  
 565 570 575  
 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe  
 580 585 590  
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His  
 595 600 605

<210> 98

<211> 65

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC20187

<400> 98

tcaccacgcg aattcggtac cgctggttcc gcgtggatcc tgccccgacc tcgtctgcta 60  
 caccg 65

<210> 99

<211> 68

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC20185

<400> 99

tctgtatcag gctgaaaatc ttatctcatc cgccaaaaca ctagtgaggg ttccagcctt 60  
 cctttaac 68

<210> 100

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC22452

<400> 100  
tcttcttggg gacactgggc c 21

<210> 101  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC22451

<400> 101  
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<210> 102  
<211> 21  
<212> DNA  
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<220>  
<223> Oligonucleotide primer ZC22450

<400> 102  
cagactaaca tgcccttcat g 21

<210> 103  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC22449

<400> 103  
ttcacttccg tgtgttctag agg 23

<210> 104  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Oligonucleotide primer ZC23771



<400> 104  
accaccttcc acaaatgc

18

<210> 105  
<211> 1347  
<212> DNA  
<213> Homo sapiens

<400> 105  
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aaaaaagagt tactcacatt catccatfff acaaagatff ccaggctgca atgggagggc 180  
tttacctctc cctgaaggat gaataaatag gtagcttaac tgacaacctg ttctcagtca 240  
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ctggcaacat ggagaggatt gtcactctgc tgatggatcat cttcttgggg aacttggtcc 360  
acaaatcaag ctcccaaggc caagatcgcc acatgattag aatgcgtcaa cttatagata 420  
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aagacattag catgattata taggagtata ctgaatttta atgaacttag cggctctaata 720  
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cctaagtagt attgctgaga cagaataaca aaactagaaa cgaaatctat actctgatca 900  
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gccttctttg ttatcctacc gaagaaacat agatacatat agtaggaagc agaattaacc 1020  
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catcccgtct ctttaagccat ttaaatccat tagagttcca ggaagaagag gcctggcatg 1260  
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<211> 1656  
<212> DNA  
<213> Homo sapiens

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gctatcagag ggaggtaccc acttcctttc tccaaaggag gggctttaat tcattttctt 180

catctgttaa	ctttacaaat	atatgttgat	cattaactgg	caagacacta	tgcctggcgc	240
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acaaatgaaa	aatgttcttc	atcagactat	aacataattt	acccaaagct	gccactagtc	360
acagtgttaag	ttttagagcc	tcataactca	gcaaatgtgt	cctaaaccga	actaactctc	420
ctttataaaa	cacaaaggct	ttgtccacca	cccagacatc	aaaatggtcc	tctgtgtagc	480
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aaactgtgag	tggtcagctt	tttcctgttt	tcagaaggcc	caactaaagt	cagcaaatac	780
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tatttgact	tataaactat	atatcttgca	ttacataaac	atacacacac	acctgtagcc	960
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acagggtttc	accatgttag	ccaggatggt	ctcgatctcc	tgaccccgtg	atccgcccgc	1260
cttggcctcc	caaagtgtgg	ggattacagg	catgagccac	cgcacccggc	ctatacgtgg	1320
tgcattttta	gaagtagggg	cactctttta	agcccacaga	cttgaaagta	ttcaaaaacc	1380
caattataat	ttcctagtag	tccttggcag	ctggaatatg	ttaatatagc	ttctcaagggt	1440
gaggaagtca	ttaggcagag	aatccaactg	tgattttgga	gttaagaact	atttcctctc	1500
atatggtcac	agataacttg	tattcttatt	aacaggagct	agatcctagc	tttctaacaa	1560
gaaaagagcc	tacaagaaga	ctagggcaaa	tcttaaaact	tgcctcctct	ctaaatcata	1620
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&lt;210&gt; 107

&lt;211&gt; 644

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

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aacgtatatc	tactatcttt	tagtgaaatg	ctctcactac	aacatcacac	tggcattgag	180
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ataaactaag	aaagcttttt	aaaaatctaa	gtgagcaatc	catatatgaa	aaactgttca	300
atctccctag	taatcacata	aatgcgagtt	aaaacaagga	aatcctgttt	tttccaatta	360
aacattttta	acaataccct	ataataataa	gaatgctcca	agtgaaaaga	ggtaaaaccc	420
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aggaatatat	caaataagca	aagatatata	tgaaaaatta	tttacagaga	tgttctttgg	540
agtaatgtag	acaaaaataa	aaagttagat	acagctgggt	gtggtggctc	atgcctgtat	600
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 <212> DNA  
 <213> Homo sapiens

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 gaaatcctgt gatatgttaa gtgtgaaaaa aaaaaagcaa atcaccaact ggtataaata 180  
 atgtaaatgc acaataataa ttaaaaatac caaaaacaca gagagaatat acattaaaac 240  
 attgcagtgg gattcctatc tctgggaatg ggattacaag gactTTTTcc attggtactt 300  
 tccaaacagt tttatgtact tctcgaatgt ttttcagtga acataattta tgTTTTaat 360  
 gaaaaaaaaa ttttaagaaac attttattac gaaaaaaatt ttaaagaaga ctgttacttt 420  
 ttcattgatt tctagacatg cccttcatgt gattcttatg agaaaaaacc acccaaagaa 480  
 ttcctagaaa gattcaaatc acttctcaa aaggtatcta ccttaagttt catttgattt 540  
 tctgctttat ctttacctat ccagatttgc ttcttagtta ctcacggtat actatttcca 600  
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<210> 109  
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<220>  
 <223> Oligonucleotide primer ZC25970

<400> 109  
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<210> 110  
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<220>  
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<400> 110  
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36

<210> 111  
<211> 153  
<212> PRT  
<213> Homo sapiens

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Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu  
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Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile  
35 40 45  
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe  
50 55 60  
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu  
65 70 75 80  
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys  
85 90 95  
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile  
100 105 110  
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala  
115 120 125  
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe  
130 135 140  
Cys Gln Ser Ile Ile Ser Thr Leu Thr  
145 150

<210> 112  
<211> 153  
<212> PRT  
<213> Homo sapiens

<400> 112  
Met Gly Leu Thr Ser Gln Leu Leu Pro Pro Leu Phe Phe Leu Leu Ala  
1 5 10 15  
Cys Ala Gly Asn Phe Val His Gly His Lys Cys Asp Ile Thr Leu Gln  
20 25 30  
Glu Ile Ile Lys Thr Leu Asn Ser Leu Thr Glu Gln Lys Thr Leu Cys  
35 40 45

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Thr Glu Leu Thr Val Thr Asp Ile Phe Ala Ala Ser Lys Asn Thr Thr
 50          55          60
Glu Lys Glu Thr Phe Cys Arg Ala Ala Thr Val Leu Arg Gln Phe Tyr
65          70          75          80
Ser His His Glu Lys Asp Thr Arg Cys Leu Gly Ala Thr Ala Gln Gln
          85          90          95
Phe His Arg His Lys Gln Leu Ile Arg Phe Leu Lys Arg Leu Asp Arg
          100          105          110
Asn Leu Trp Gly Leu Ala Gly Leu Asn Ser Cys Pro Val Lys Glu Ala
          115          120          125
Asn Gln Ser Thr Leu Glu Asn Phe Leu Glu Arg Leu Lys Thr Ile Met
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Arg Glu Lys Tyr Ser Lys Cys Ser Ser
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<210> 113
<211> 162
<212> PRT
<213> Homo sapiens

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Val Phe Ile Leu Gly Cys Phe Ser Ala Gly Leu Pro Lys Thr Glu Ala
          35          40          45
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
          50          55          60
Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
65          70          75          80
Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
          85          90          95
Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
          100          105          110
Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
          115          120          125
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
          130          135          140
Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
145          150          155          160
Thr Ser

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<210> 114  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
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 20 25 30  
 Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp  
 35 40 45  
 Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe  
 50 55 60  
 Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys  
 65 70 75 80  
 Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met  
 85 90 95  
 Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
 100 105 110  
 Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys  
 115 120 125  
 Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu  
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<210> 115  
 <211> 538  
 <212> PRT  
 <213> Homo sapiens

<400> 115  
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 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr  
 20 25 30  
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr  
 35 40 45  
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser  
 50 55 60  
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr  
 65 70 75 80

Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
				85					90					95	
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
			100					105					110		
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
		115					120					125			
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp
	130					135				140					
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
145				150						155					160
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile
				165					170					175	
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys
			180					185					190		
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
		195					200					205			
Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
	210					215					220				
Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu
225					230					235					240
Leu	Leu	Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys
				245					250					255	
Thr	His	Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser
			260					265					270		
Pro	Glu	Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe
		275					280					285			
Lys	Lys	Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly
	290					295					300				
Pro	Trp	Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His
305					310					315					320
Pro	Pro	Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu
				325					330					335	
Pro	Ala	Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp
			340					345					350		
Pro	Thr	Ala	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp
		355					360					365			
Arg	Pro	Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Leu	Asp	Ala
	370					375					380				
Glu	Gly	Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro
385					390					395					400
Ala	Leu	Asp	Leu	Asp	Ala	Gly	Leu	Glu	Pro	Ser	Pro	Gly	Leu	Glu	Asp
				405					410					415	

